

sequence_listing.txt

10/547532

SEQUENCE LISTING

<110> SHINTANI, ET AL.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.1USWO

<140> New filing

<141> August 31, 2005

<150> PCT/JP2004/002774

<151> 2004-03-04

<150> JP 2003-056885

<151> 2003-03-04

<150> JP 2003-106247

<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(288)

<223>

<220>

<221> sig_peptide

<222> (1)..(78)

<223>

<220>

<221> mat_peptide

<222> (79)..()

<223>

<400> 1

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atg tgc tgt acc aag agt ttg ctc ctg gct gct ttg atg tca gtg ctg      48Met Cys Cys
Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu      -25
-20      -15      cta ctc cac ctc tgc ggc gaa tca gaa
gca gca agc aac ttt gac tgc      96Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser
Asn Phe Asp Cys      -10      -5      -1 1      5
      tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc
144Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
10      15      20      ttc aca cgg cag ctg
gcc aat gaa ggc tgt gac atc aat gct atc atc      192Phe Thr Arg Gln Leu Ala Asn Glu
Gly Cys Asp Ile Asn Ala Ile Ile      25      30
35      ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa
cag act      240Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
40      45      50      tgg gtg aaa
tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg      288Trp val Lys Tyr Ile val
Arg Leu Leu Ser Lys Lys Val Lys Asn Met      55      60
65      70

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<210> 2
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Cys Cys Thr Lys Ser Leu Leu Ala Ala Leu Met Ser Val Leu
 -25 -20 -15
 Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys
 -10 -5 -1 1 5
 Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly
 10 15 20
 Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile
 25 30 35
 Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr
 40 45 50
 Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met
 55 60 65 70

<210> 3
 <211> 288
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (1)..(288)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(75)
 <223>

<220>
 <221> mat_peptide
 <222> (76)..()
 <223>

<400> 3
 atg gcc tgc aag cat ctg ccc ttc ctg gct ttg gcg ggg gta ctg ctg 48Met Ala Cys
 Lys His Leu Pro Phe Leu Ala Leu Ala Gly Val Leu Leu -25 -20
 -15 -10
 gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc 96Ala Tyr Leu
 Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys -5
 -1 1 5
 cat gcg aga aat ttt gtg ggt 144Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg
 Asn Phe Val Gly 10 15 20
 ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct atc atc
 192Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile 25
 30 35
 aaa aga tcc gtg tgc gct gac cca aag cag atc 240Phe His Leu Lys Ser Lys Arg Ser
 Val Cys Ala Asp Pro Lys Gln Ile 40 45 50
 55
 aag atg 288Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met
 60 65 70

<210> 4
 <211> 96
 <212> PRT
 <213> Rattus norvegicus

<400> 4

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Met Ala Cys Lys His Leu Pro Phe Leu Ala Leu Ala Gly Val Leu Leu
-25 -20 -15 -10
Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys
-5 -1 1 5
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly
10 15 20
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile
25 30 35
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile
40 45 50 55
Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met
60 65 70

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<210> 5
 <211> 291
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(291)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(81)
 <223>

<220>
 <221> mat_peptide
 <222> (82)..()
 <223>

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<400> 5
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Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val -25
-20 -15 ctg ctg gct cac ctc tgc agc cag gca
gaa gca gca agc aac tac gac 96Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala
Ser Asn Tyr Asp -10 -5 -1 1
5 tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg
144Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
10 15 20 ggt ttc aca aga cag
atg gcc gat gaa gct tgt gac att aat gct atc 192Gly Phe Thr Arg Gln Met Ala Asp
Glu Ala Cys Asp Ile Asn Ala Ile 25 30
35 atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca
aag cag 240Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
40 45 50 aac tgg
gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag 288Asn Trp Val Lys Arg
Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys 55 60
65 atg
291Met
70

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<210> 6
 <211> 97
 <212> PRT
 <213> Mus musculus

<400> 6
 Met Ala Cys Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val
 -25 -20 -15
 Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp

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```

-10          -5          -1  1          5
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val
      10      15      20
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile
      25      30      35
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln
      40      45      50
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys
      55      60      65
Met
70

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<210> 7
<211> 1122
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(1122)
<223>

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<400> 7
atg agc ggg gaa tca atg aat ttc agc gat gtt ttc gac tcc agt gaa      48Met Ser Gly
Glu Ser Met Asn Phe Ser Asp Val Phe Asp Ser Ser Glu      1      5
      10      15      20      25      30
tat tac tca gtt gat tct gag      96Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser
Val Asp Ser Glu      20      25      30
      35      40      45      50      55
atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta ttt
144Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
35      40      45      50      55
tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat      192Val Pro Ile Ala Tyr Ser Leu Ile
Cys Val Phe Gly Leu Leu Gly Asn      50      55
60      65      70      75      80
tct atg      240Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65      70      75      80      85
gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt      288Thr Asp Val Tyr Leu
Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val      85      90
90      95      100      105      110
act ggt gcg tgg gtt      336Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala
Trp Val      100      105      110      115
      120      125      130      135      140
ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc aac      384Phe Ser
Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn      115      120
120      125      130      135      140
act tgc att agc atg gac cgg tac      432Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile
Ser Met Asp Arg Tyr      130      135      140      145
      150      155      160      165      170
atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc      528Leu Pro Arg Ser Lys Ile Ile Cys
Leu Val Val Trp Gly Leu Ser Val      165      170      175
175      180      185      190      195
acc caa      576Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
180      185      190      195      200
gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc      624Gly Ser Asp Val Cys
Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile      195      200
205      210      215      220      225
ctc ttt ggt ttc ttt      672Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly
Phe Phe      210      215      220      225
      230      235      240      245      250
atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att gtc aaa acc      720Ile Pro
Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr      225      230
230      235      240      245      250
agg cac aaa gcc atc cgt gta atc      768Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys
      240      245      250

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Ala Ile Arg Val Ile
255      ata gct gtg gtg ctt gtg ttt ctg gct tgt cag att cct cat aac atg
816Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
260      265      270      gtc ctg ctt gtg acg
gct gca aat ttg ggt aaa atg aac cga tcc tgc      864Val Leu Leu Val Thr Ala Ala Asn
Leu Gly Lys Met Asn Arg Ser Cys      275      280
285      cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa
gtc ctg      912Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
290      295      300      gct ttc
ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg      960Ala Phe Leu His Cys
Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly      305      310
315      320      cag aag ttc aga aac tac ttt ctg aag atc ttg
aag gac ctg tgg tgt      1008Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu
Trp Cys      325      330      335
gtg aga agg aag tac aag tcc tca ggc ttc tcc tgt gcc ggg agg tac      1056Val Arg
Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr      340
345      350      tca gaa aac att tct cgg cag acc
agt gag acc gca gat aac gac aat      1104Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr
Ala Asp Asn Asp Asn      355      360      365
1122Ala Ser Ser Phe Thr Met

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370

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<210> 8
<211> 374
<212> PRT
<213> Homo sapiens

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```

<400> 8
Met Ser Gly Glu Ser Met Asn Phe Ser Asp Val Phe Asp Ser Ser Glu
1      5      10      15
Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu
20      25      30
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
35      40      45
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
50      55      60
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65      70      75      80
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
85      90      95
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
100      105      110
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
115      120      125
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
130      135      140
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145      150      155      160
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
165      170      175
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
180      185      190
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
195      200      205
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Gly Phe Phe
210      215      220
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225      230      235      240
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
245      250      255
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
260      265      270

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Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
 275 280 285
 Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
 290 295 300
 Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
 305 310 315 320
 Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
 325 330 335
 Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
 340 345 350
 Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn
 355 360 365
 Ala Ser Ser Phe Thr Met
 370

<210> 9
 <211> 1101
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1101)
 <223>

<400> 9

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 Thr Glu Ser Tyr Phe Gly Thr Asp Asp Tyr Asp Asn Thr 1 5
 10 15 gag tat tat tct att cct cca gac cat
 ggg cca tgc tcc cta gaa gag 96Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys
 Ser Leu Glu Glu 20 25 30
 gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta ata
 144Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
 35 40 45 50 55
 ctg ggc aac att atg gtg gtg atg acc ttt gcc 192Cys Val Phe Gly Leu Leu Gly Asn
 Ile Met Val Val Met Thr Phe Ala 50 55
 60 ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg ttg
 aac atg 240Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75 80 85
 aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288Ala Ile Thr Asp Ile
 Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val 85
 90 95 act cat gcc acc aac act tgg gtt ttc agc gat
 gca ctg tgt aaa ctg 336Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys
 Lys Leu 100 105 110
 atg aaa ggc aca tat gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg 384Met Lys
 Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu 115
 120 125 gcc tgt atc agc atg gac cgg tac
 att gcc atc gtc cag gca acc aaa 432Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile
 Val Gln Ala Thr Lys 130 135 140
 tct ttc cgg gta cgc tcc aga aca ctg acg cac agt aag gtc atc tgt
 480Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys 145
 150 155 160 165 170
 atc tcc atc atc atc tca agc cct aca ttt atc 528Val Ala Val Trp Phe Ile Ser Ile
 Ile Ile Ser Ser Pro Thr Phe Ile 165 170
 175 ttc aac aag aaa tac gag ctg cag gat cgt gat gtc tgt gag
 cca cgg 576Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
 180 185 190 195 200
 tct gtc tca gag ccc atc acg tgg aag ctg ctg ggt atg gga 624Tyr Arg Ser Val Ser
 Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly 195 200
 205 ctg gag ctg ttc ttt ggg ttc ttc acc cct ttg
 ctg ttt atg gtg ttc 672Leu Glu Leu Phe Phe Gly Phe Phe Thr Pro Leu Leu Phe Met
 Val Phe 210 215 220
 tgc tat ctg ttc att atc aag acc ttg gtg cag gcc cag aac tcc aag 720Cys Tyr

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Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys 225
230 235 240 245 250
atc gct gtg gtt ctc gtg ttc ctg 768Arg His Arg Ala Ile Arg Val Val Ile Ala Val
Val Leu Val Phe Leu 255
255 gct tgt cag atc cct cac aac atg gtc ctc ctc gtg act gcg gtc aac
816Ala Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Val Asn
260 265 270
cgg agc tgc agc acc gag aaa gtc ctc gcc tac 864Thr Gly Lys Val Gly Arg Ser Cys
Ser Thr Glu Lys Val Leu Ala Tyr 275 280
285 acc agg aac gtg gcc gag gtc ctg gct ttc ctg cat tgc tgc
ctc aac 912Thr Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn
290 295 300
ttg tat gcg ttt att gga cag aaa ttc aga aac tac ttc atg 960Pro Val Leu Tyr Ala
Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Met 305 310
315 320
aag aat aag atg cct 1008Lys Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys
Met Pro 325 330 335
ggc ttc ctc tgt gcc cgg gtt tac tcg gaa agc tac atc tcc agg cag 1056Gly Phe
Leu Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln 340
345 350
aat gca tcg tcc ttt acc atg 1101Thr Ser Glu Thr Val Glu Asn Asp Asn Ala Ser
Ser Phe Thr Met 355 360 365

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<210> 10
 <211> 367
 <212> PRT
 <213> Mus musculus

<400> 10

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Met Asn Ser Thr Glu Ser Tyr Phe Gly Thr Asp Asp Tyr Asp Asn Thr
1 5 10 15
Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
20 25 30
Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
35 40 45
Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
50 55 60
Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
65 70 75 80
Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
85 90 95
Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
100 105 110
Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
115 120 125
Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys
130 135 140
Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys
145 150 155 160
Val Ala Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
165 170 175
Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
180 185 190
Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly
195 200 205
Leu Glu Leu Phe Phe Gly Phe Phe Thr Pro Leu Leu Phe Met Val Phe
210 215 220
Cys Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys
225 230 235 240
Arg His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu
245 250 255
Ala Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Val Asn

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```

                260
Thr Gly Lys Val Gly Arg Ser Cys Ser Thr Glu Lys Val Leu Ala Tyr
                270
                275
Thr Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn
                285
                290
Pro Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Met
                300
                305
Lys Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro
                310
                315
Gly Phe Leu Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln
                320
                325
Thr Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met
                330
                335
                340
                345
                350
                355
                360
                365

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<210> 11
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> misc_feature
 <223> Oligonucleotide designed to act as primer for amplifying fragment of
 rat MIP-3f₂ gene transcript.

<400> 11
 agaatggcct gcaagcatct 20

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> misc_feature
 <223> Oligonucleotide designed to act as primer for amplifying fragment of
 rat MIP-3f₂ gene transcript.

<400> 12
 tgcagaggta agccagcagt a 21

<210> 13
 <211> 1502
 <212> DNA
 <213> Rattus norvegicus (kidney)

<220>
 <221> CDS
 <222> (343)..(1443)
 <223>

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<400> 13
tgtattgaag acagaacact tgttgtaaga caccaccccc cgggagggcg aagaacaagc 60cacacactgc
tttgaagagt ccagcccca gcagaactgc aagggcagac actgttctgg 120ccacctgcag tttgaagtca
tcactttcaa tccccctgtg actagggcca gggctctcac 180acctgcgaga ggaagcaaag atctaagcaa
tctgaatttt aagagagaaa ctgcagctgt 240cggtttgtgg gccggaacat tattggactg gagcctggac
aagcactaag gcgggggtac 300ctggccagcc cacttcggag ctacgcgttt ccttgggaaa cg atg aat
ttc acc 354 Met Asn Phe Thr
aag ggc tca gat tac tct atg 1
aac tac gga atg gaa gat tat act ggc tca gat tac tct atg 402Glu Ala Asn Tyr Gly
Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met 5
15 20 ttt cca gag acc gag cca tgc tct ctg caa gag
gtc aga gac ttc acc 450Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val Arg Asp
Phe Thr 25 30 35

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sequence_listing.txt

```

aag gtg ttc gtg cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc      498Lys Val
Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu      40
45      50      ctt ggc aat att atg gtg gtg ata
acc ttt gcc ttc tac aag aaa gcc      546Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala
Phe Tyr Lys Lys Ala      55      60      65
agg tcc atg act gac gtc tac cta ttg aac atg gcc atc aca gac ata
594Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile      70
75      80      ctc ttt gtc ctc acc
cta cca ttc tgg gca gtt act cat gcc act gac      642Leu Phe Val Leu Thr Leu Pro Phe
Trp Ala Val Thr His Ala Thr Asp      85      90      95
100      act tgg atc ttt ggc aac acg atg tgt aaa ctg atg aaa ggc
acg tat      690Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met Lys Gly Thr Tyr
105      110      115      gcg gtc
aac ttt aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg      738Ala Val Asn Phe Asn
Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met      120
125      130      gac cgg tac att gcc atc gtc cag gcg acc aaa
tct ttc cgg gta cgc      786Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg
Val Arg      135      140      145
tcc aga aca ctg acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc      834Ser Arg
Thr Leu Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe      150
155      160      gtt tcc atc atc atc tca agc ccc
aca ttc ttc ttc aac aag caa tac      882Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe
Phe Asn Lys Gln Tyr      165      170      175
180      aag ctg cag ggc cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg
930Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser
185      190      195      gag ccc atc acg tgg
aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt      978Glu Pro Ile Thr Trp Lys Leu Leu
Gly Met Gly Leu Glu Leu Leu Phe      200      205
210      ggc ttc ttc atc cct ttg ctg ttt atg gtg ttc tgt tac ctg
ttc atc      1026Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile
215      220      225      atc aag
acc ttg gtg cag gcc cag aat tcc aag agg cac aga gcc atc      1074Ile Lys Thr Leu Val
Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile      230      235
240      cga gtc gtg att gct gtg gtt ctc gtg ttc ctg
gct tgt cag atc cct      1122Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln
Ile Pro      245      250      255      260
cac aac atg gtc ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc      1170His Asn
Met Val Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly      265
270      275      cgc agc tgc agc gcc gag aaa gcc
ctc gcc tac gcc agg aat gtg gct      1218Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr
Ala Arg Asn Val Ala      280      285      290
gag gtc ctg gct ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc
1266Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala
295      300      305      ttc att gga cag aaa
ttc aga agc tac ttc atg aag atc atg aag gat      1314Phe Ile Gly Gln Lys Phe Arg Ser
Tyr Phe Met Lys Ile Met Lys Asp      310      315
320      gtg tgg tgt atg agg agg aag agc aag gtg cct acc ttc ttc
tgt gcc      1362Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys Ala
325      330      335      340      cgg gtt
tac tca gaa agc tac atc tcc agg cag acc agt gag act gta      1410Arg Val Tyr Ser Glu
Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val      345
350      355      gaa aat gac aac gca tcg tcc ttt acc atg taa
cacgagagca caaagcagca      1463Glu Asn Asp Asn Ala Ser Ser Phe Thr Met
360      365
tgccccgaaa gcctttgtga aacttgctat tacatgtga      1502

```

<210> 14
 <211> 366
 <212> PRT
 <213> Rattus norvegicus

<400> 14
 Met Asn Phe Thr Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser

sequence_listing.txt

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1      5      10      15
Asp Tyr Ser Met Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val
20      30
Arg Asp Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys
35      40      45
Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe
50      55      60
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
65      70      75      80
Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr
85      90      95
His Ala Thr Asp Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met
100      105      110
Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Ala
115      120      125
Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
130      135      140
Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu
145      150      155      160
Thr Val Trp Phe Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe Phe
165      170      175
Asn Lys Gln Tyr Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr
180      185
Lys Leu Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu
195      200      205
Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys
210      215      220
Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg
225      230      235      240
His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala
245      250      255
Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Thr
260      265      270
Gly Lys Met Gly Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr Ala
275      280      285
Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro
290      295      300
Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Ser Tyr Phe Met Lys
305      310      315      320
Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr
325      330      335
Phe Phe Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr
340      345      350
Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met
355      360      365

```

```

<210> 15
<211> 1309
<212> DNA
<213> Rattus norvegicus (liver)

```

```

<220>
<221> CDS
<222> (150)..(1250)
<223>

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<400> 15
gcattctcact acccgctctct caatgagcac cgctgggttgt gcctgtcaac agaatagtcc 60tctcacactt
aggactggag cctggacaag cactaaggcg ggggtacctg gccagcccac 120ttcggagctc agcgtttctt
tgaggaaacg atg aat ttc acc gag gcc aac tac 173
Met Asn Phe Thr Glu Ala Asn Tyr
5      1
gga atg gaa gat tat act ggc tca gat tac tct atg ttt cca
gag acc 221Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met Phe Pro Glu Thr

```

sequence_listing.txt

```

10          15          20          gag cca
tgc tct ctg caa gag gtc aga gac ttc acc aag gtg ttc gtg      269Glu Pro Cys Ser Leu
Gln Glu Val Arg Asp Phe Thr Lys Val Phe Val      25      30
35          40          50          cca atc gcc tac tcc tta atc tgt gtc ttt ggc
ctc ctt ggc aat att      317Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly
Asn Ile      45      55
atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc agg tcc atg act      365Met Val
Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met Thr      60
65          70          gac gtc tac cta ttg aac atg gcc
atc aca gac ata ctc ttt gtc ctc      413Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp
Ile Leu Phe Val Leu      75      80      85
acc cta cca ttc tgg gca gtt act cat gcc act gac act tgg atc ttt
461Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp Thr Trp Ile Phe      90
95          100          ggc aac acg atg tgt
aaa ctg atg aaa ggc acg tat gcg gtc aac ttt      509Gly Asn Thr Met Cys Lys Leu Met
Lys Gly Thr Tyr Ala Val Asn Phe      105      110      115
120          aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg gac cgg
tac att      557Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met Asp Arg Tyr Ile
125          130          135          gcc atc
gtc cag gcg acc aaa tct ttc cgg gta cgc tcc aga aca ctg      605Ala Ile Val Gln Ala
Thr Lys Ser Phe Arg Val Arg Ser Arg Thr Leu      140
145          150          acg cac agt aag gtc atc tgt ctg acg gtg tgg
ttc gtt tcc atc atc      653Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe Val Ser
Ile Ile      155      160      165
atc tca agc ccc aca ttc ttc ttc aac aag caa tac aag ctg cag ggc      701Ile Ser
Ser Pro Thr Phe Phe Phe Asn Lys Gln Tyr Lys Leu Gln Gly      170
175          180          cgt gat gtc tgc gag cct cag tac
aag ctc gtc tcg gag ccc atc acg      749Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val
Ser Glu Pro Ile Thr      185      190      195
200          tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt ggc ttc ttc atc
797Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe Gly Phe Phe Ile
205          210          215          cct ttg ctg ttt atg
gtg ttc tgt tac ctg ttc atc atc aag acc ttg      845Pro Leu Leu Phe Met Val Phe Cys
Tyr Leu Phe Ile Ile Lys Thr Leu      220      225
230          gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc
gtg att      893Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile
235          240          245          gct gtg
gtt ctc gtg ttc ctg gct tgt cag atc cct cac aac atg gtc      941Ala Val Val Leu Val
Phe Leu Ala Cys Gln Ile Pro His Asn Met Val      250      255
260          ctc ctc gtg act gca gcc aac acg ggc aaa atg
ggc cgc agc tgc agc      989Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser
Cys Ser      265      270      275      280
gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct      1037Ala Glu
Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala      285
290          295          ttc ctg cac tgc tgt ctc aac ccc
gtg ttg tat gcc ttc att gga cag      1085Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr
Ala Phe Ile Gly Gln      300      305      310
aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt atg
1133Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met
315          320          325          agg agg aag agc aag
gtg cct acc ttc ttc tgt gcc cgg gtt tac tca      1181Arg Arg Lys Ser Lys Val Pro Thr
Phe Phe Cys Ala Arg Val Tyr Ser      330      335
340          gaa agc tac atc tcc agg cag acc agt gag act gta gaa aat
gac aac      1229Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp Asn
345          350          355          gca tcg
tcc ttt acc atg taa cacgagagca caaagcagca tgccccgaaa      1280Ala Ser Ser Phe Thr
Met      365

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gcctttgtga aacttgctat tacatgtga

1309

<210> 16
<211> 25
<212> DNA

sequence_listing.txt

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<213> Artificial

<220>
<223> oligonucleotide designed to act as primer for amplifying CCR6
      cDNA derived from rat kidney.

<400> 16
tgtattgaag acagaacact tgtgg                                25

<210> 17
<211> 28
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide designed to act as primer for amplifying CCR6
      cDNA derived from rat kidney or rat liver.

<400> 17
tcacatgtaa tagcaagttt caciaagg                                28

<210> 18
<211> 21
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide designed to act as primer for amplifying CCR6
      cDNA derived from rat liver.

<400> 18
gcatctcact acccgctctct c                                    21

<210> 19
<211> 21
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide designed to act as primer for amplifying fragment      of
      rat CCR6 gene transcript.

<400> 19
ggacgatgcg ttgtcatttt c                                    21

<210> 20
<211> 22
<212> DNA
<213> Artificial

<220>
<223> oligonucleotide designed to act as primer for amplifying fragment      of
      rat CCR6 gene transcript.

<400> 20
ccgcagctgc agcgccgaga aa                                    22

<210> 21
<211> 20
<212> DNA
<213> Artificial

<220>

```

<223> Oligonucleotide designed to act as primer for amplifying fragment of
rat CCR6 gene transcript.

<400> 21

gtgcccgggt ttactcagaa

20